

SQL Le A 36 269

SEQUENCE LISTING

<110> Bayer AG, BHC

<120> Method for inhibiting the replication of herpesviruses

<130> Le A 36 269

<160> 1

<170> PatentIn version 3.1

<210> 1

<211> 1370

<212> PRT

<213> Human cytomegalovirus

<400> 1

Met Glu Asn Trp Ser Ala Leu Glu Leu Leu Pro Lys Val Gly Ile Pro
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 Thr Asp Phe Leu Thr His Val Lys Thr Ser Ala Gly Glu Glu Met Phe
 20 25 30
 Glu Ala Leu Arg Ile Tyr Tyr Gly Asp Asp Pro Glu Arg Tyr Asn Ile
 35 40 45
 His Phe Glu Ala Ile Phe Gly Thr Phe Cys Asn Arg Leu Glu Trp Val
 50 55 60
 Tyr Phe Leu Thr Ser Gly Leu Ala Ala Ala His Ala Ile Lys Phe
 65 70 75 80
 His Asp Leu Asn Lys Leu Thr Thr Gly Lys Met Leu Phe His Val Gln
 85 90 95
 Val Pro Arg Val Ala Ser Gly Ala Gly Leu Pro Thr Ser Arg Gln Thr
 100 105 110
 Thr Ile Met Val Thr Lys Tyr Ser Glu Lys Ser Pro Ile Thr Ile Pro
 115 120 125
 Phe Glu Leu Ser Ala Ala Cys Leu Thr Tyr Leu Arg Glu Thr Phe Glu
 130 135 140
 Gly Thr Ile Leu Asp Lys Ile Leu Asn Val Glu Ala Met His Thr Val
 145 150 155 160
 Leu Arg Ala Leu Lys Asn Thr Ala Asp Ala Met Glu Arg Gly Leu Ile
 165 170 175
 His Ser Phe Leu Gln Thr Leu Leu Arg Lys Ala Pro Pro Tyr Phe Val
 180 185 190
 Val Gln Thr Leu Val Glu Asn Ala Thr Leu Ala Arg Gln Ala Leu Asn
 195 200 205
 Arg Ile Gln Arg Ser Asn Ile Leu Gln Ser Phe Lys Ala Lys Met Leu
 210 215 220
 Ala Thr Leu Phe Leu Leu Asn Arg Thr Arg Asp Arg Asp Tyr Val Leu
 225 230 235 240
 Lys Phe Leu Thr Arg Leu Ala Glu Ala Ala Thr Asp Ser Ile Leu Asp
 245 250 255
 Asn Pro Thr Thr Tyr Thr Ser Ser Gly Ala Lys Ile Ser Gly Val
 260 265 270
 Met Val Ser Thr Ala Asn Val Met Gln Ile Ile Met Ser Leu Leu Ser
 275 280 285
 Ser His Ile Thr Lys Glu Thr Val Ser Ala Pro Ala Thr Tyr Gly Asn
 290 295 300
 Phe Val Leu Ser Pro Glu Asn Ala Val Thr Ala Ile Ser Tyr His Ser
 305 310 315 320
 Ile Leu Ala Asp Phe Asn Ser Tyr Lys Ala His Leu Thr Ser Gly Gln
 325 330 335
 Pro His Leu Pro Asn Asp Ser Leu Ser Gln Ala Gly Ala His Ser Leu
 340 345 350
 Thr Pro Leu Ser Met Asp Val Ile Arg Leu Gly Glu Lys Thr Val Ile

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355	Met Glu Asn Leu Arg Arg Val	360	Tyr Lys Asn Thr Asp Thr Lys Asp Pro	365		
370	375	380	385	390	395	400
Leu Glu Arg Asn Val Asp Leu Thr Phe Phe Phe Pro Val Gly Leu Tyr	405	410	415	420	425	430
Leu Pro Glu Asp Arg Gly Tyr Thr Thr Val Glu Ser Lys Val Lys Leu	435	440	445	450	455	460
Asn Asp Thr Val Arg Asn Ala Leu Pro Thr Thr Ala Tyr Leu Leu Asn	475	480	485	490	495	500
Arg Asp Arg Ala Val Gln Lys Ile Asp Phe Val Asp Ala Leu Lys Thr	515	520	525	530	535	540
Leu Cys His Pro Val Leu His Glu Pro Ala Pro Cys Leu Gln Thr Phe	550	555	560	565	570	575
Thr Glu Arg Gly Pro Pro Ser Glu Pro Ala Met Gln Arg Leu Leu Glu	580	585	590	595	600	605
Cys Arg Phe Gln Gln Glu Pro Met Gly Gly Ala Ala Arg Arg Ile Pro	610	615	620	625	630	635
His Phe Tyr Arg Val Arg Arg Glu Val Pro Arg Thr Val Asn Glu Met	640	645	650	655	660	665
Lys Gln Asp Phe Val Val Thr Asp Phe Tyr Lys Val Gly Asn Ile Thr	675	680	685	690	695	700
Leu Tyr Thr Glu Leu His Pro Phe Asp Phe Thr His Cys Gln Glu	710	715	720	725	730	735
Asn Ser Glu Thr Val Ala Leu Cys Thr Pro Arg Ile Val Ile Gly Asn	740	745	750	755	760	765
Leu Pro Asp Gly Leu Ala Pro Gly Pro Phe His Glu Leu Arg Thr Trp	770	775	780	785	790	795
Glu Ile Met Glu His Met Arg Leu Arg Pro Pro Pro Asp Tyr Glu Glu	800	805	810	815	820	825
Thr Leu Arg Leu Phe Lys Thr Thr Val Thr Ser Pro Asn Tyr Pro Glu	830	835	840	845	850	855
Leu Cys Tyr Leu Val Asp Val Leu Val His Gly Asn Val Asp Ala Phe	860	865	870	875	880	885
Leu Leu Ile Arg Thr Phe Val Ala Arg Cys Ile Val Asn Met Phe His	890	895	900	905	910	915
Thr Arg Gln Leu Leu Val Phe Ala His Ser Tyr Ala Leu Val Thr Leu	920	925	930	935	940	945
Ile Ala Glu His Leu Ala Asp Gly Ala Leu Pro Pro Gln Leu Leu Phe	950	955	960	965	970	975
His Tyr Arg Asn Leu Val Ala Val Leu Arg Leu Val Thr Arg Ile Ser	980	985	990	995	1000	1005
Ala Leu Pro Gly Leu Asn Asn Gln Leu Ala Glu Glu Pro Leu Ser	1010	1015	1020	1025	1030	1035
Ala Tyr Val Asn Ala Leu His Asp His Arg Leu Trp Pro Pro Phe Val	1040	1045	1050	1055	1060	1065
Thr His Leu Pro Arg Asn Met Glu Gly Val Gln Val Val Ala Asp Arg	1070	1075	1080	1085	1090	1095
Gln Pro Leu Asn Pro Ala Asn Ile Glu Ala Arg His His Gly Val Ser	1100	1105	1110	1115	1120	1125
Asp Val Pro Arg Leu Gly Ala Met Asp Ala Asp Glu Pro Leu Phe Val	1130	1135	1140	1145	1150	1155
Asp Asp Tyr Arg Ala Thr Asp Asp Glu Trp Thr Leu Gln Lys Val Phe	1160	1165	1170	1175	1180	1185
Tyr Leu Cys Leu Met Pro Ala Met Thr Asn Asn Arg Ala Cys Gly Leu	1190	1195	1200	1205	1210	1215
Gly Leu Asn Leu Lys Thr Leu Leu Val Asp Leu Phe Tyr Arg Pro Ala	1220	1225	1230	1235	1240	1245
Phe Leu Leu Met Pro Ala Ala Thr Ala Val Ser Thr Ser Gly Thr Thr	1250	1255	1260	1265	1270	1275
Ser Lys Glu Ser Thr Ser Gly Val Thr Pro Glu Asp Ser Ile Ala Ala	1280	1285	1290	1295	1300	1305
Gln Arg Gln Ala Val Gly Glu Met Leu Thr Glu Leu Val Glu Asp Val	1310	1315	1320	1325	1330	1335

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Ala	Thr	Asp	Ala	His	Thr	Pro	Leu	Leu	Gln	Ala	Cys	Arg	Glu	Leu	Phe
865					870				875						880
Leu	Ala	Val	Gln	Phe	Val	Gly	Glu	His	Val	Lys	Val	Leu	Glu	Val	Arg
						885			890						895
Ala	Pro	Leu	Asp	His	Ala	Gln	Arg	Gln	Gly	Leu	Pro	Asp	Phe	Ile	Ser
					900			905						910	
Arg	Gln	His	Val	Leu	Tyr	Asn	Gly	Cys	Cys	Val	Val	Thr	Ala	Pro	Lys
					915			920						925	
Thr	Leu	Ile	Glu	Tyr	Ser	Leu	Pro	Val	Pro	Phe	His	Arg	Phe	Tyr	Ser
					930			935					940		
Asn	Pro	Thr	Ile	Cys	Ala	Ala	Leu	Ser	Asp	Asp	Ile	Lys	Arg	Tyr	Val
945					950				955						960
Thr	Glu	Phe	Pro	His	Tyr	His	Arg	His	Asp	Gly	Gly	Phe	Pro	Leu	Pro
					965			970						975	
Thr	Ala	Phe	Ala	His	Glu	Tyr	His	Asn	Trp	Leu	Arg	Ser	Pro	Phe	Ser
					980			985						990	
Arg	Tyr	Ser	Ala	Thr	Cys	Pro	Asn	Val	Leu	His	Ser	Val	Met	Thr	Leu
								995	1000				1005		
Ala	Ala	Met	Leu	Tyr	Lys	Ile	Ser	Pro	Val	Ser	Leu	Val	Leu	Gln	
						1010		1015				1020			
Thr	Lys	Ala	His	Ile	His	Pro	Gly	Phe	Ala	Leu	Thr	Ala	Val	Arg	
						1025		1030				1035			
Thr	Asp	Thr	Phe	Glu	Val	Asp	Met	Leu	Leu	Tyr	Ser	Gly	Lys	Ser	
					1040		1045				1050				
Cys	Thr	Ser	Val	Ile	Ile	Asn	Asn	Pro	Ile	Val	Thr	Lys	Glu	Glu	
					1055		1060				1065				
Arg	Asp	Ile	Ser	Thr	Thr	Tyr	His	Val	Thr	Gln	Asn	Ile	Asn	Thr	
					1070		1075				1080				
Val	Asp	Met	Gly	Leu	Gly	Tyr	Thr	Ser	Asn	Thr	Cys	Val	Ala	Tyr	
					1085		1090				1095				
Val	Asn	Arg	Val	Arg	Thr	Asp	Met	Gly	Val	Arg	Val	Gln	Asp	Leu	
					1100		1105				1110				
Phe	Arg	Val	Phe	Pro	Met	Asn	Val	Tyr	Arg	His	Asp	Glu	Val	Asp	
					1115		1120				1125				
Arg	Trp	Ile	Arg	His	Ala	Ala	Gly	Val	Glu	Arg	Pro	Gln	Leu	Leu	
					1130		1135				1140				
Asp	Thr	Glu	Thr	Ile	Ser	Met	Leu	Thr	Phe	Gly	Ser	Met	Ser	Glu	
					1145		1150				1155				
Arg	Asn	Ala	Ala	Ala	Thr	Val	His	Gly	Gln	Lys	Ala	Ala	Cys	Glu	
					1160		1165				1170				
Leu	Ile	Leu	Thr	Pro	Val	Thr	Met	Asp	Val	Asn	Tyr	Phe	Lys	Ile	
					1175		1180				1185				
Pro	Asn	Asn	Pro	Arg	Gly	Arg	Ala	Ser	Cys	Met	Leu	Ala	Val	Asp	
					1190		1195				1200				
Pro	Tyr	Asp	Thr	Glu	Ala	Ala	Thr	Lys	Ala	Ile	Tyr	Asp	His	Arg	
					1205		1210				1215				
Glu	Ala	Asp	Ala	Gln	Thr	Phe	Ala	Ala	Thr	His	Asn	Pro	Trp	Ala	
					1220		1225				1230				
Ser	Gln	Ala	Gly	Cys	Leu	Ser	Asp	Val	Leu	Tyr	Asn	Thr	Arg	His	
					1235		1240				1245				
Arg	Glu	Arg	Leu	Gly	Tyr	Asn	Ser	Lys	Phe	Tyr	Ser	Pro	Cys	Ala	
					1250		1255				1260				
Gln	Tyr	Phe	Asn	Thr	Glu	Glu	Ile	Ile	Ala	Ala	Asn	Lys	Thr	Leu	
					1265		1270				1275				
Phe	Lys	Thr	Ile	Asp	Glu	Tyr	Leu	Leu	Arg	Ala	Lys	Asp	Cys	Ile	
					1280		1285				1290				
Arg	Gly	Asp	Thr	Asp	Thr	Gln	Tyr	Val	Cys	Val	Glu	Gly	Thr	Glu	
					1295		1300				1305				
Gln	Leu	Ile	Glu	Asn	Pro	Cys	Arg	Leu	Thr	Gln	Glu	Ala	Leu	Pro	
					1310		1315				1320				
Ile	Leu	Ser	Thr	Thr	Thr	Leu	Ala	Leu	Met	Glu	Thr	Lys	Leu	Lys	
					1325		1330				1335				
Gly	Gly	Ala	Gly	Ala	Phe	Ala	Thr	Ser	Glu	Thr	His	Phe	Gly	Asn	

Le A 36 269-Foreign countries

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